

RAW SEQUENCE LISTING

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Application Serial Number: 10/536, 606
Source: PCT
Date Processed by STIC: 03/06/2006

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PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/536,606

DATE: 03/06/2006
TIME: 15:17:43

Input Set : A:\25421-502NATL.txt
Output Set: N:\CRF4\03062006\J536606.raw

3 <110> APPLICANT: Cosson et al.
 5 <120> TITLE OF INVENTION: VIRULENCE GENES, PROTEINS, AND THEIR USE
 7 <130> FILE REFERENCE: 25421-502NATL
 9 <140> CURRENT APPLICATION NUMBER: 10/536,606
 10 <141> CURRENT FILING DATE: 2005-05-26
 12 <150> PRIOR APPLICATION NUMBER: PCT/CH2003/00836
 13 <151> PRIOR FILING DATE: 2003-12-19
 15 <150> PRIOR APPLICATION NUMBER: 10/324,967
 16 <151> PRIOR FILING DATE: 2002-12-19
 18 <160> NUMBER OF SEQ ID NOS: 64
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1050
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Pseudomonas aeruginosa
 27 <400> SEQUENCE: 1
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 30 atgcaggcgg tcatgcgcca gatcatgacc gggcagtgc cccacgcgca gatccggcgcc 120
 32 ttccctgatgg gcatgcggat gaagagcgaa accatcgacg agatcgctgg cgccgtggcg 180
 34 gtatgcgcg aactggccga cggcgtgcag ttgcctacgc tgaagcatgt ggtgcacgtg 240
 36 gtcggcaccc gcgccgatgg cgccgaacatc ttcaacgtgt ctcggcgcc gtccttcgtg 300
 38 gtcggcccg ctggcgccaa ggtcgccaaa cacggtaacc ggcgggtctc cggcaagagc 360
 40 ggcagcgccg acttgctgga agccgcggc atctacctgg agctgaccc tcgaacaggtg 420
 42 ggcgttgca tcgacaccgt cgccgtcggtt ttcatgttgc cccaggtcca ccacaaggcg 480
 44 atgaagtacg ccgcgggtcc ggcgcgcgag ctgggttgc ggactctgtt caacatgctt 540
 46 ggcccaactga ccaacccggc gggagtcagg caccaggtgg tcgggggtttt caccaggaa 600
 48 ctgtgcaagc cgctggctga atgtctcaag cgtctcgca ggcggcatgt gctgggtgt 660
 50 cattcgccgc acgggctgga cgagttcagt ctggccgcgg cgacccacat tgccgagttg 720
 52 aaggacggcg aggtacgcga gtacgaagtgc cgtcccgagg acttcgggat caagagccag 780
 54 accctgatgg ggctggaggt cgacagtccg caggcctcg tggaaactgtat ccgcgacgct 840
 56 ttggggcgcc gcaagaccga ggctggcag aaggccgcg agctgatgt gatgaatgcc 900
 58 ggcccgacac tgcacaccgg gctggcacgg gagaagatgg acgaactggt ggccttcacc 960
 60 cacatgccc tgcacaccgg gctggcacgg gagaagatgg acgaactggt ggccttcacc 1020
 62 ggcgttaca gagaggagaa cgacagtga 1050
 65 <210> SEQ ID NO: 2
 66 <211> LENGTH: 349
 67 <212> TYPE: PRT
 68 <213> ORGANISM: Pseudomonas aeruginosa
 70 <400> SEQUENCE: 2
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 73 1 5 10 15
 76 Thr Thr Glu Glu Met Gln Ala Val Met Arg Gln Ile Met Thr Gly Gln
 77 20 25 30

CPG-6)

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80 Cys Thr Asp Ala Gln Ile Gly Ala Phe Leu Met Gly Met Arg Met Lys
81 35 40 45
84 Ser Glu Thr Ile Asp Glu Ile Val Gly Ala Val Ala Val Met Arg Glu
85 50 55 60
88 Leu Ala Asp Gly Val Gln Leu Pro Thr Leu Lys His Val Val Asp Val
89 65 70 75 80
92 Val Gly Thr Gly Asp Gly Ala Asn Ile Phe Asn Val Ser Ser Ala
93 85 90 95
96 Ala Ser Phe Val Val Ala Ala Gly Gly Lys Val Ala Lys His Gly
97 100 105 110
100 Asn Arg Ala Val Ser Gly Lys Ser Gly Ser Ala Asp Leu Leu Glu Ala
101 115 120 125
104 Ala Gly Ile Tyr Leu Glu Leu Thr Ser Glu Gln Val Ala Arg Cys Ile
105 130 135 140
108 Asp Thr Val Gly Val Gly Phe Met Phe Ala Gln Val His His Lys Ala
109 145 150 155 160
112 Met Lys Tyr Ala Ala Gly Pro Arg Arg Glu Leu Gly Leu Arg Thr Leu
113 165 170 175
116 Phe Asn Met Leu Gly Pro Leu Thr Asn Pro Ala Gly Val Arg His Gln
117 180 185 190
120 Val Val Gly Val Phe Thr Gln Glu Leu Cys Lys Pro Leu Ala Glu Val
121 195 200 205
124 Leu Lys Arg Leu Gly Ser Glu His Val Leu Val Val His Ser Arg Asp
125 210 215 220
128 Gly Leu Asp Glu Phe Ser Leu Ala Ala Ala Thr His Ile Ala Glu Leu
129 225 230 235 240
132 Lys Asp Gly Glu Val Arg Glu Tyr Glu Val Arg Pro Glu Asp Phe Gly
133 245 250 255
136 Ile Lys Ser Gln Thr Leu Met Gly Leu Glu Val Asp Ser Pro Gln Ala
137 260 265 270
140 Ser Leu Glu Leu Ile Arg Asp Ala Leu Gly Arg Arg Lys Thr Glu Ala
141 275 280 285
144 Gly Gln Lys Ala Ala Glu Leu Ile Val Met Asn Ala Gly Pro Ala Leu
145 290 295 300
148 Tyr Ala Ala Asp Leu Ala Thr Ser Leu His Glu Gly Ile Gln Leu Ala
149 305 310 315 320
152 His Asp Ala Leu His Thr Gly Leu Ala Arg Glu Lys Met Asp Glu Leu
153 325 330 335
156 Val Ala Phe Thr Ala Val Tyr Arg Glu Glu Asn Ala Gln
157 340 345
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161 <211> LENGTH: 918
162 <212> TYPE: DNA
163 <213> ORGANISM: Pseudomonas aeruginosa
165 <400> SEQUENCE: 3
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168 gaggtggccg ccgagttcga taacccgggt atgctgtact cgatcgccaa ggattccgcg 120
170 gtcatgctgc acctggcccg caaggccttc ttcccccggca agctgccctt cccgggtatg 180
172 cacgtggaca cccgctggaa attccaggag atgtacaggt tccgtgatcg gatggtcgag 240

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174 gaaatgggcc tggatctgtat caccacgtc aaccggacg gcgtcgccca gggcatcaac 300
 176 ccgttcaccc acggcagcgc caagcacacc gacgtatga agaccgaggg actcaagcag 360
 178 gccctggaca agtacggttt cgacgctgcc ttcggcggtg cgccgcgca cgaggagaag 420
 180 tcgcgggcca aggaacgggtt ctattcggtc cgccgacagca agcaccgctg ggaccgcgaa 480
 182 aaccagcgtc ccgagctgtg gaacatctac aacggcaagg tgaagaaggg cgagtcgatc 540
 184 cgcttcccgatcgatccaa ctggaccgag ctggacatct ggcaatacat ctacctggaa 600
 186 ggcatcccga tcgtcccgct gtacttcgccc gccgagcgcg aggtcatcga gaagaatggc 660
 188 acattgatca tgatcgacga cgagcgcattc ctcgagcatc tctctgacga agagaaagcc 720
 190 cgcattcgaga agcgcattgtt ggcgttccgtt accctcggtt gctacccgtt caccggcgcg 780
 192 gtcgagtcac ggcgcaccac gtcggcggaa atcatccagg aaatgtctctt gacgcgtact 840
 194 tccgaacgccc agggccgggtt catcgaccat gaccaggccg gttcgatgga agaaaagaaa 900
 196 cgtcagggtt atttctgt 918
 199 <210> SEQ ID NO: 4
 200 <211> LENGTH: 305
 201 <212> TYPE: PRT
 202 <213> ORGANISM: *Pseudomonas aeruginosa*
 204 <400> SEQUENCE: 4
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 207 1 5 10 15
 210 His Ile Ile Arg Glu Val Ala Ala Glu Phe Asp Asn Pro Val Met Leu
 211 20 25 30
 214 Tyr Ser Ile Gly Lys Asp Ser Ala Val Met Leu His Leu Ala Arg Lys
 215 35 40 45
 218 Ala Phe Phe Pro Gly Lys Leu Pro Phe Pro Val Met His Val Asp Thr
 219 50 55 60
 222 Arg Trp Lys Phe Gln Glu Met Tyr Arg Phe Arg Asp Arg Met Val Glu
 223 65 70 75 80
 226 Glu Met Gly Leu Asp Leu Ile Thr His Val Asn Pro Asp Gly Val Ala
 227 85 90 95
 230 Gln Gly Ile Asn Pro Phe Thr His Gly Ser Ala Lys His Thr Asp Val
 231 100 105 110
 234 Met Lys Thr Glu Gly Leu Lys Gln Ala Leu Asp Lys Tyr Gly Phe Asp
 235 115 120 125
 238 Ala Ala Phe Gly Gly Ala Arg Arg Asp Glu Glu Lys Ser Arg Ala Lys
 239 130 135 140
 242 Glu Arg Val Tyr Ser Phe Arg Asp Ser Lys His Arg Trp Asp Pro Lys
 243 145 150 155 160
 246 Asn Gln Arg Pro Glu Leu Trp Asn Ile Tyr Asn Gly Lys Val Lys Lys
 247 165 170 175
 250 Gly Glu Ser Ile Arg Val Phe Pro Leu Ser Asn Trp Thr Glu Leu Asp
 251 180 185 190
 254 Ile Trp Gln Tyr Ile Tyr Leu Glu Gly Ile Pro Ile Val Pro Leu Tyr
 255 195 200 205
 258 Phe Ala Ala Glu Arg Glu Val Ile Glu Lys Asn Gly Thr Leu Ile Met
 259 210 215 220
 262 Ile Asp Asp Glu Arg Ile Leu Glu His Leu Ser Asp Glu Glu Lys Ala
 263 225 230 235 240
 266 Arg Ile Glu Lys Arg Met Val Arg Phe Arg Thr Leu Gly Cys Tyr Pro
 267 245 250 255

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270 Leu Thr Gly Ala Val Glu Ser Ser Ala Thr Thr Leu Pro Glu Ile Ile
 271 260 265 270
 274 Gln Glu Met Leu Leu Thr Arg Thr Ser Glu Arg Gln Gly Arg Val Ile
 275 275 280 285
 278 Asp His Asp Gln Ala Gly Ser Met Glu Glu Lys Lys Arg Gln Gly Tyr
 279 290 295 300

282 Phe

283 305

286 <210> SEQ ID NO: 5

287 <211> LENGTH: 822

288 <212> TYPE: DNA

289 <213> ORGANISM: Pseudomonas aeruginosa

291 <400> SEQUENCE: 5

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 294 ctggccgact ggccgcggca cgtgggtggc cgctcgaagg ccgacgaatc gccgggtgact 120
 296 gccgcccggacc tggccgcgc ccatatattt gaggcggtat tgccggcgct ggccgcggac 180
 298 attccgggtgc ttcccaaga ggattgcgag ataccgctga gcgagcgcgg ccactggcg 240
 300 cgctgggtggc tggtgacccc gctggacggc accaaggagt tcatctccgg tagcgaggag 300
 302 ttccaccgtca acgtggccct ggtcgaggat ggccgggtgc tggatggcct ggtcgccgtg 360
 304 ccgggtgagcg gcccgtgcta ctacgggtggc gccggctctcg tggatggcct ggaggaggcc 420
 306 gatggccgcg cgcacccgat cagtgtgcgc ctggagcccg aggaggcctt caccgtggtg 480
 308 gccagcaagg gccatggcag cccggcccaag gagccctgc tggatggcctt gagcgagcgc 540
 310 ttccggcgacc tgcggcgagc cagcatcgcc agttcgctga agttctgcct gtcggccgag 600
 312 ggcgctgccc actgtatcc ggcgctgacg ccaacctcgc aatgggacac ggccgcggcc 660
 314 cagggtgtgc tggaaaggcgc cggcgccgag gtgctcgacc tgcatggtgc gccattcacc 720
 316 tacgagccgc gcgaggattt cctcaacggc tccttcctgg ccctgcccgg cgccgcggag 780
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321 <210> SEQ ID NO: 6

322 <211> LENGTH: 273

323 <212> TYPE: PRT

324 <213> ORGANISM: Pseudomonas aeruginosa

326 <400> SEQUENCE: 6

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 332 Gly Glu Ala Ile Leu Pro His Trp Arg Ala Asp Val Val Val Arg Ser
 333 20 25 30
 336 Lys Ala Asp Glu Ser Pro Val Thr Ala Ala Asp Leu Ala Ala His His
 337 35 40 45
 340 Ile Leu Glu Ala Gly Leu Arg Ala Leu Ala Pro Asp Ile Pro Val Leu
 341 50 55 60
 344 Ser Glu Glu Asp Cys Glu Ile Pro Leu Ser Glu Arg Gly His Trp Arg
 345 65 70 75 80
 348 Arg Trp Trp Leu Val Asp Pro Leu Asp Gly Thr Lys Glu Phe Ile Ser
 349 85 90 95
 352 Gly Ser Glu Glu Phe Thr Val Asn Val Ala Leu Val Glu Asp Gly Arg
 353 100 105 110
 356 Val Leu Phe Gly Leu Val Gly Val Pro Val Ser Gly Arg Cys Tyr Tyr
 357 115 120 125
 360 Gly Gly Ala Gly Leu Gly Ala Trp Arg Glu Glu Ala Asp Gly Arg Ala

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361	130	135	140													
364	Gln	Pro	Ile	Ser	Val	Arg	Leu	Glu	Pro	Glu	Glu	Ala	Phe	Thr	Val	Val
365	145				150				155						160	
368	Ala	Ser	Lys	Arg	His	Gly	Ser	Pro	Ala	Gln	Glu	Arg	Leu	Leu	Asp	Gly
369						165				170					175	
372	Leu	Ser	Glu	Arg	Phe	Gly	Asp	Leu	Arg	Arg	Ala	Ser	Ile	Gly	Ser	Ser
373						180			185					190		
376	Leu	Lys	Phe	Cys	Leu	Leu	Ala	Glu	Gly	Ala	Ala	Asp	Cys	Tyr	Pro	Arg
377						195			200					205		
380	Leu	Thr	Pro	Thr	Ser	Gln	Trp	Asp	Thr	Ala	Ala	Ala	Gln	Gly	Val	Leu
381						210			215					220		
384	Glu	Gly	Ala	Gly	Gly	Glu	Val	Leu	Asp	Leu	His	Gly	Ala	Pro	Phe	Thr
385	225					230				235					240	
388	Tyr	Glu	Pro	Arg	Glu	Asp	Tyr	Leu	Asn	Gly	Ser	Phe	Leu	Ala	Leu	Pro
389						245				250					255	
392	Arg	Ala	Ala	Glu	Trp	Arg	Ser	Glu	Leu	Ile	Gln	Leu	Ala	Arg	Ala	Leu
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396	His															
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402	<212>	TYPE:	DNA													
403	<213>	ORGANISM:	Pseudomonas	aeruginosa												
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410	ttcgccaaacg	ccggccagggt	gtctcccggt	tacgcttcgc	cctgggcagc	cccgggcatt									180	
412	ccccctgaagg	ccatgaagtg	gctgctggaa	aagcacgcgc	cgctggccat	caagctcacc									240	
414	tccgatccca	gccagtagcgc	ctggatgtcg	cagatgtgc	gcaactgcac	cggcgagcgc									300	
416	tacggcgtga	acaaggagcg	catggtccgc	ctgtccgagt	acagccgcga	ttgcctcgac									360	
418	gaactgcgcg	ccgagaccgg	catgcctac	gaggccgcga	ccctccggcac	cacccaactg									420	
420	ttccgcaccc	aggcgcagct	ggacgcccgc	ggcaaggaca	tcgcccgtct	cgagcgctcc									480	
422	ggcgtgcct	acgaggttct	cgaccgcgcac	ggcatcgccc	gcgttagagcc	ggctttggcc									540	
424	aagggtgcgcg	acaagctgtt	ccggcgccttg	cgcctgccc	acgaccagac	cggcgactgc									600	
426	cagctgttca	ccacccgcct	ggcgaaaatg	gccaaggggcc	tgggcgttga	tttccgcgttc									660	
428	ggccagaaca	tcgagcgcct	ggacttcgccc	ggcgaccgcac	tcaacggcggt	gttgtcaac									720	
430	ggcgaattgc	tcaccgcgc	ccactacgtg	ctggccctgg	gcagctactc	gccgcaactg									780	
432	ctcaagccgc	tgggtatcaa	ggctccggtc	tatccgtga	agggttattc	gtgaccgtg									840	
434	ccgatcacca	acccggagat	ggcgccgcacc	tcgaccatcc	tcgacgagac	ctacaagggt									900	
436	gcatcacc	gttgcacca	gcatccgc	gtcggcggca	tggcggaaat	cggcgcttc									960	
438	gacctgtcgc	tgaacccgcg	ccggcgcgcag	accctggaaa	tgatcaccac	cgacccctat									1020	
440	cccgaggggcg	gcatatccat	ccaggcgacc	ttctggaccg	gcctgcgccc	ggcgaccccg									1080	
442	gatggcacc	cgatcgctgg	cgccacccgc	taccgcaacc	tgttcctcaa	taccggccac									1140	
444	ggcacccctgg	gttggaccat	ggcctgcggg	tcgggtcgct	acctggccga	cctgatggcg									1200	
446	aagaagcgcc	cgcagatcg	taccgaaggc	ctggatattt	cccgctacag	caattccccg									1260	
448	gagaacgcca	agaatcccc	tccagcgcca	gcacactaa											1299	
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452	<211>	LENGTH:	432													
453	<212>	TYPE:	PRT													
454	<213>	ORGANISM:	Pseudomonas	aeruginosa												

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:37; N Pos. 85,88,174,175,245,293,319,325

VERIFICATION SUMMARY

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L:4828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:60

M:341 Repeated in SeqNo=37